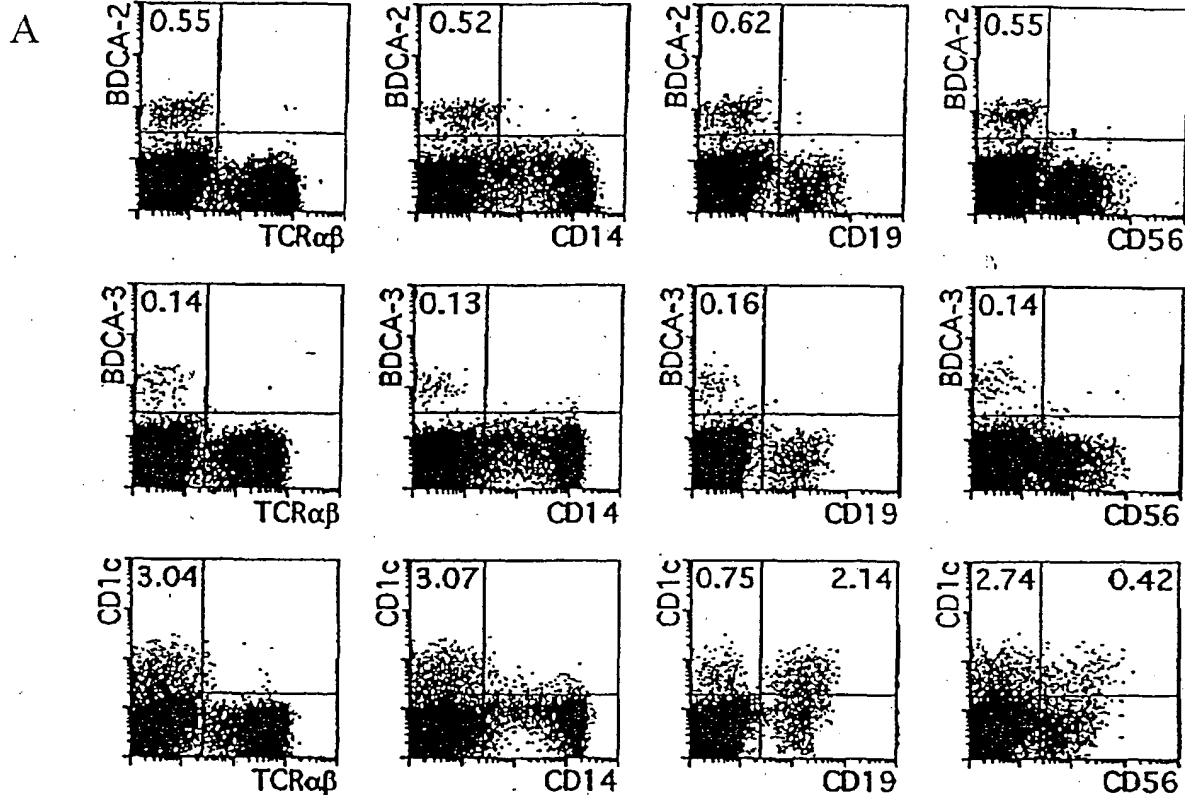


FIGURE 1



B

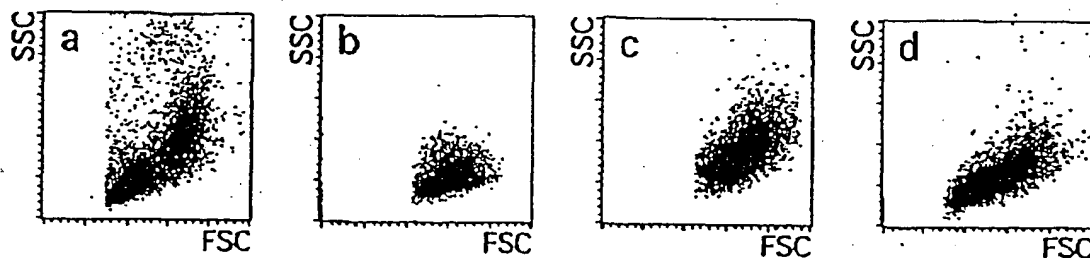


FIGURE 2

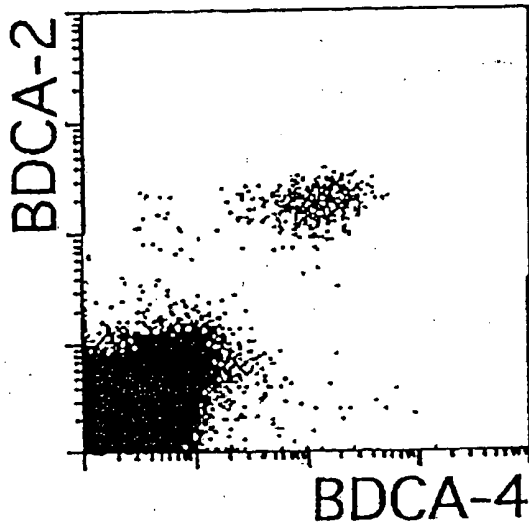


FIGURE 3

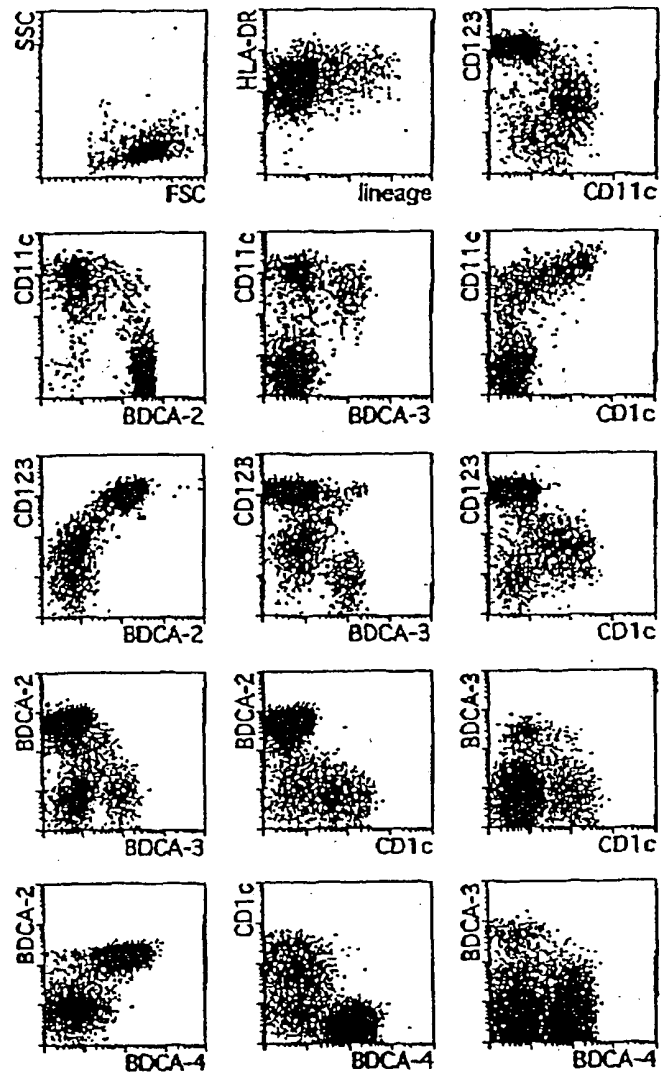
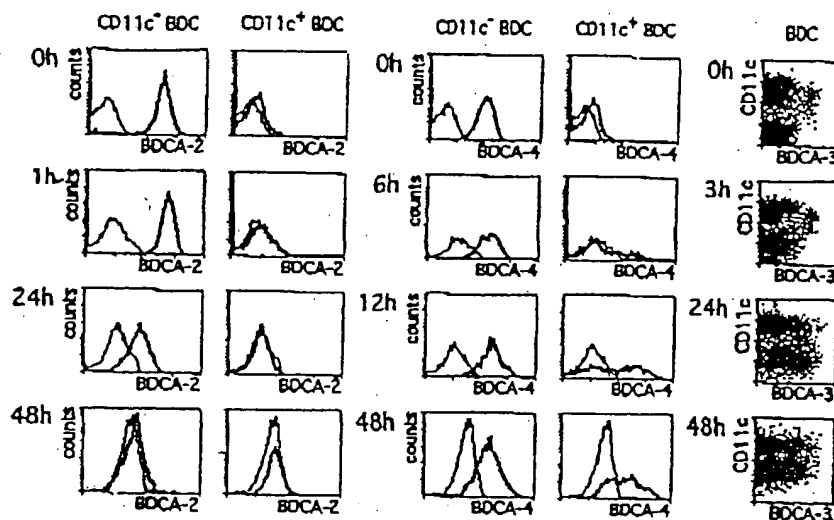


FIGURE 4

A



B

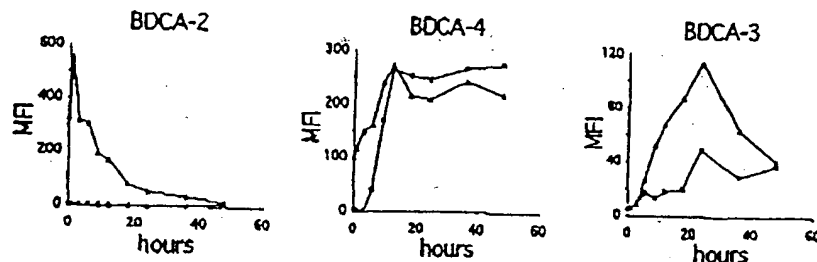


FIGURE 5

MVPEEEEPQDREKGLWWFQLKVWSMAVVSILLLSVCFTVSSVVPHNFMYS
 KTVKRLSKLREYQQYHPSLTCVMEGKDIEDWSCCPTPWTSFQSSCYFISTG
 MQSWTKSQKNCSVMGADLVVINTREEQDFIIQNLRNSSYFLGLSDPGGR
 RHWQWVDQTPYNENVTFWHSGEPPNNLDERCAIINFRSSEEWGWNDIHCH
 VPQKSICKMKKIYI (SEQ ID NO:2)



FIGURE 6

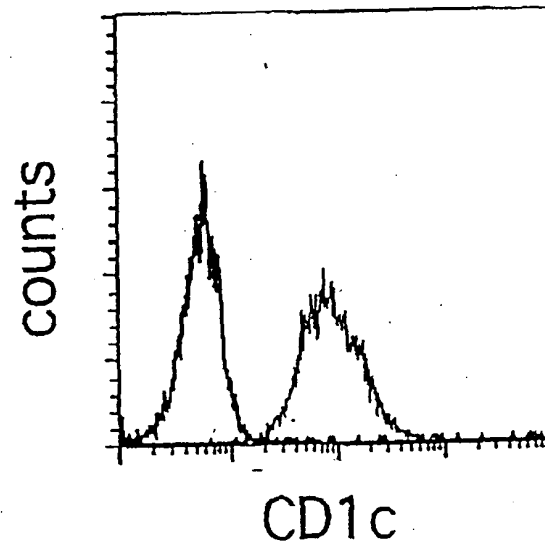


FIGURE 7

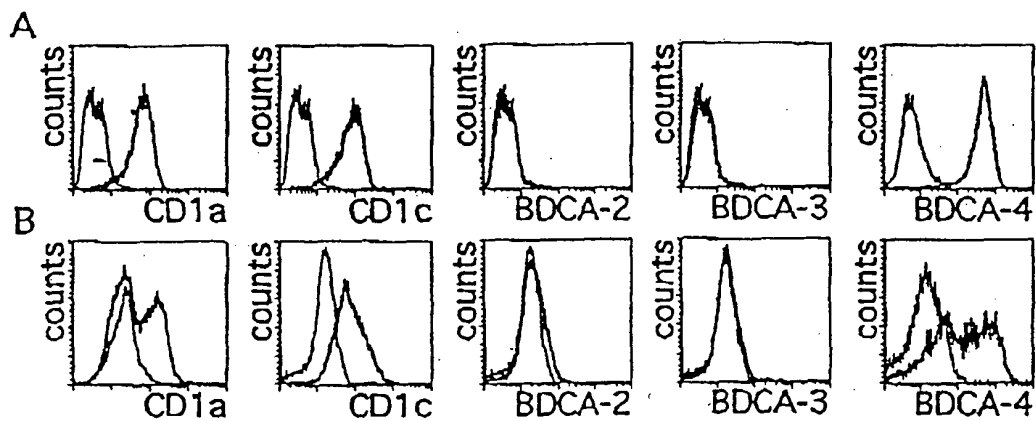


FIGURE 8

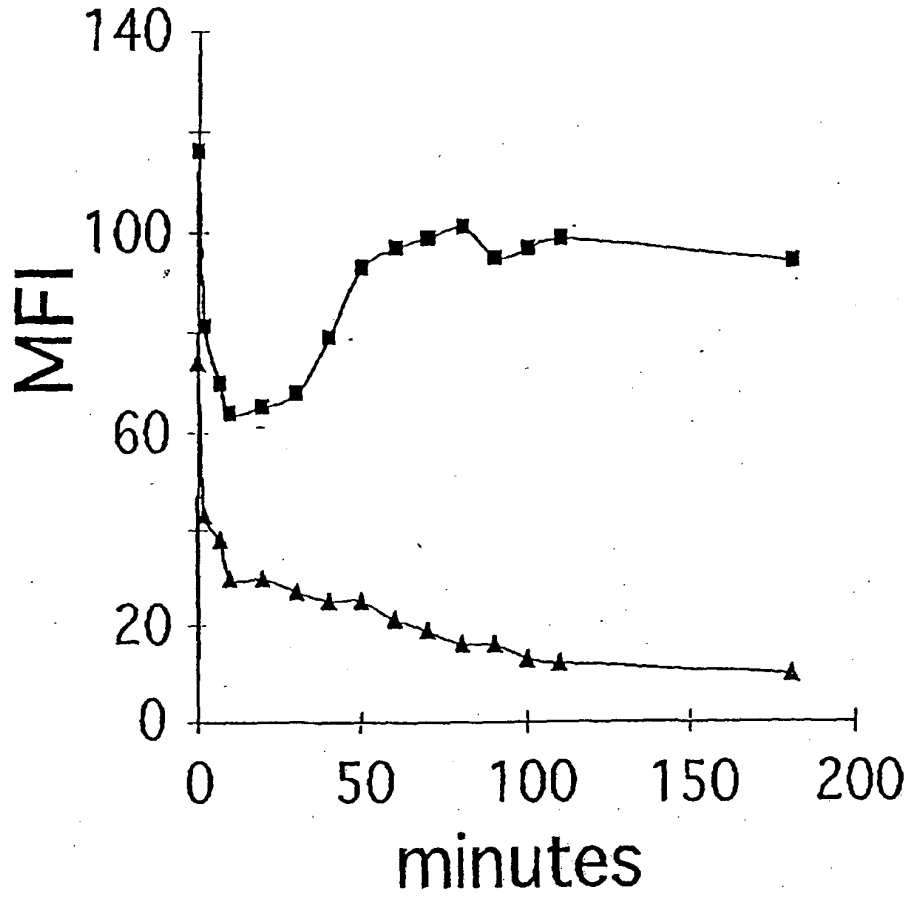


FIGURE 9

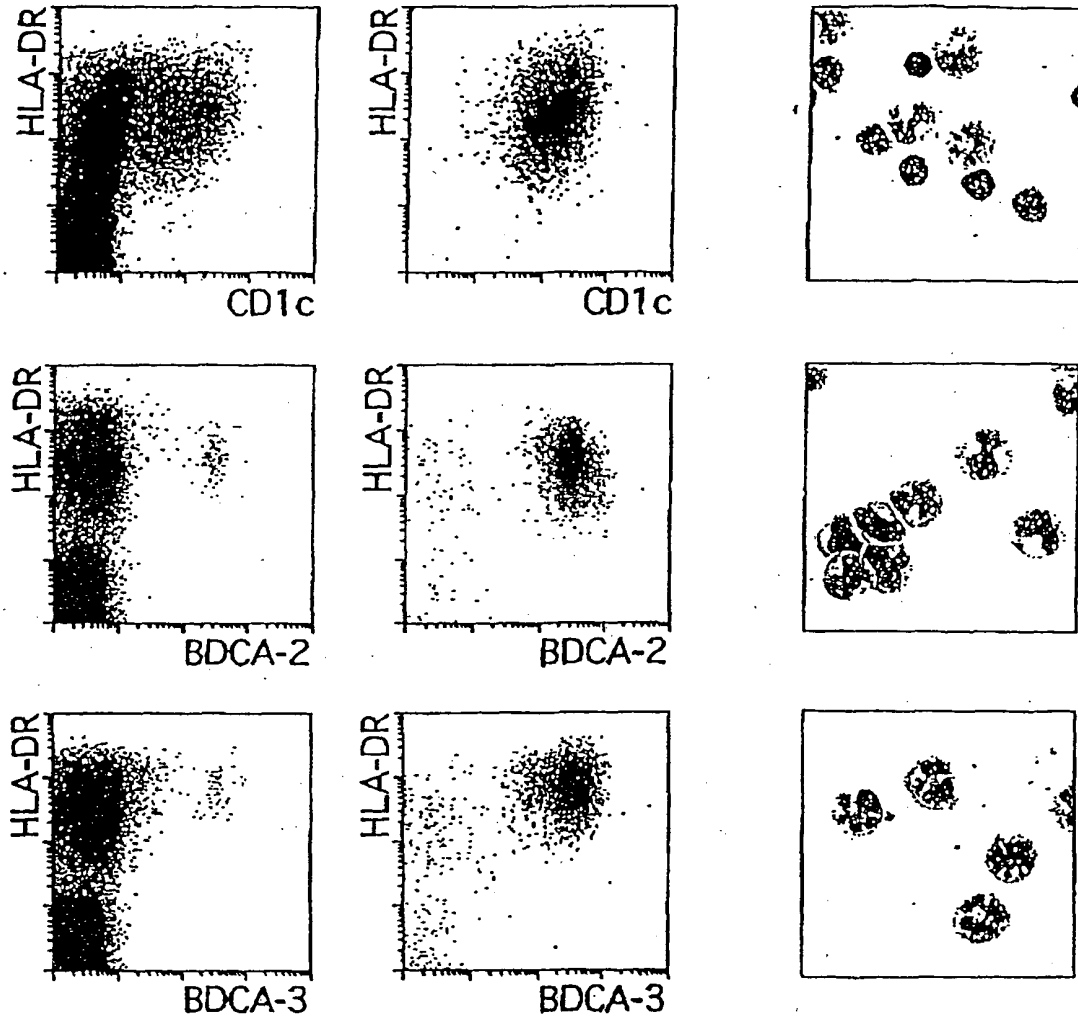


FIGURE 10

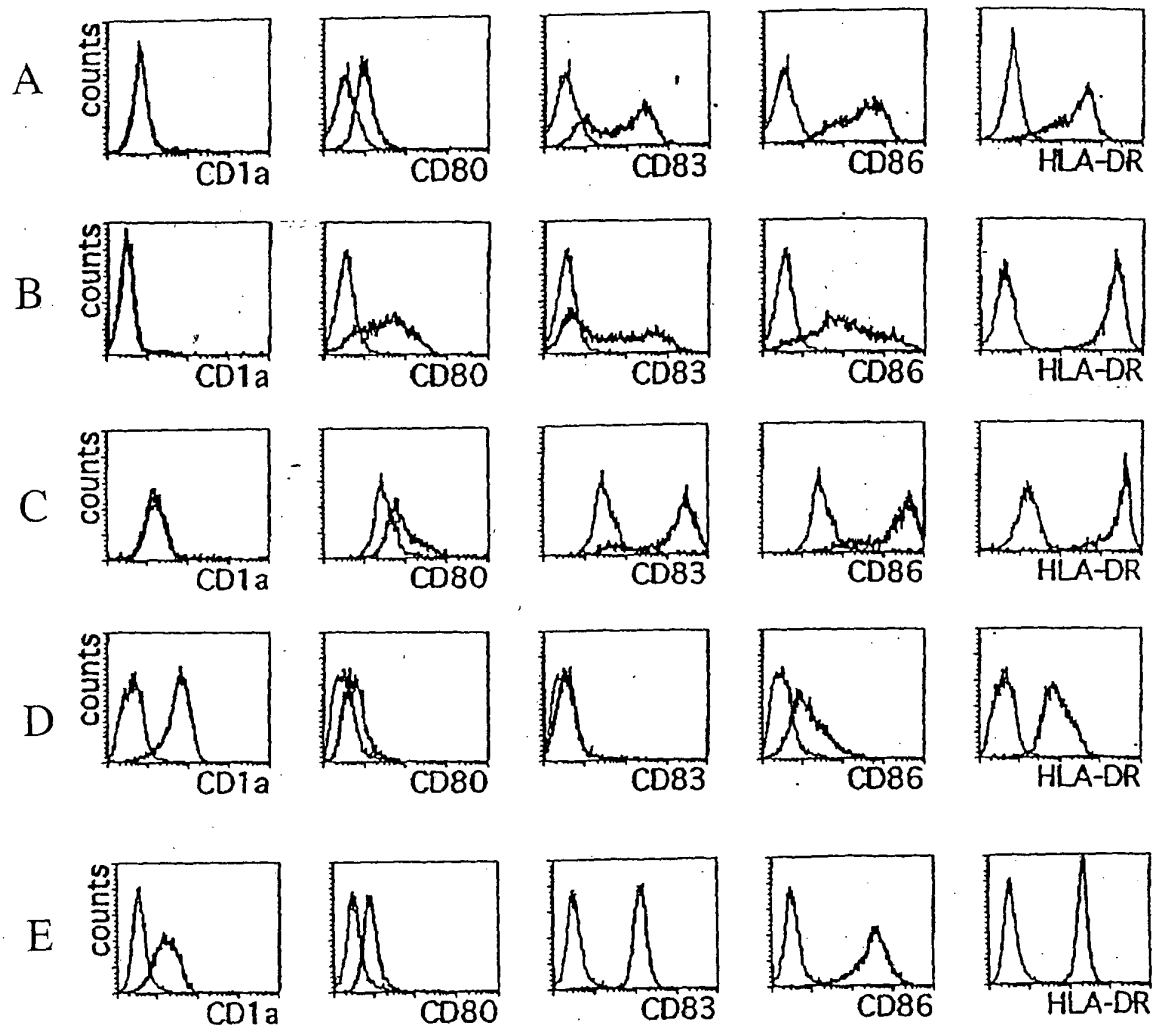


FIGURE 11

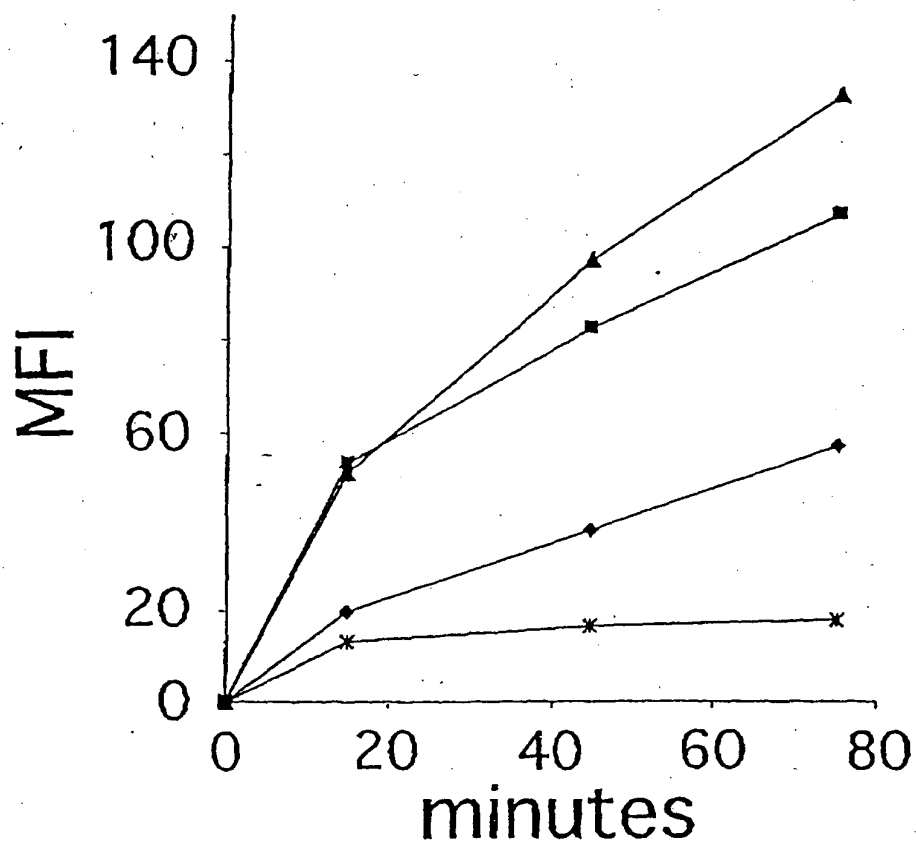


FIGURE 12

CAGTGATTCTCGTGCCTCAGCCTCCTGAGTAGCCGAAATTACAGACGTG
TGCCACCATGCTTGGCTAATTTTTTGGATTTTATAGTAGAGATGGGGTTTC
ACTATGTTGGCCAGGCTAGTCTTGAACCTCCTGGCCTGAAGCAATCCGCC
CACCTCAGCCTCCCAAAGTGCTGAGATTATAGGCACGAGCCACTACAC
CTGGCCACAAAATTCTTTAAAGAAGCCAATCCCATCCTCCCTCAAGAGC
CAAGGGGCCACCTCACCTCTTGTTACAGCAGATCCTGCCTCCACAGTC
ACCCTGCTCCCAAGTGCAACCTCTGTCTGACCCTGCATGGTGTGCGGTG
CCCTCCTGCCTCAGGCCGCGAAGAAGGATCTAAGGGCTTGGCTTGTTTG
AAAGAACCACACCCCGAAAGTAACATCTTTGGAGAAAGTGATACAAGA
GCTTCTGCACCCACCTGATAGAGGAAGTCCAAAGGGTGTGCGCACACA
CAATGGTGCCTGAAGAAGAGCCTCAAGACCGAGAGAAAGGACTCTGGT
GGTTCCAGTTGAAGGTCTGGTCCATGGCAGTCGTATCCATCTTGCTCCT
CAGTGTCTGTTTCACTGTGAGTTCTGTGGTGCCTCACAATTTTATGTATA
GCAAAACTGTCAAGAGGCTGTCCAAGTTACGAGAGTATCAACAGTATC
ATCCAAGCCTGACCTGCGTCATGGAAGGAAAGGACATAGAAGATTGGA
GCTGCTGCCCAACCCCTTGGACTTCATTTCACTAGTTGCTACTTTATT
TCTACTGGGATGCAATCTTGGACTAAGAGTCAAAAGAACTGTTCTGTGA
TGGGGGCTGATCTGGTGGTGTGATCAACACCAGGGAAGAACAGGATTTCA
TCATTCAGAATCTGAAAAGAAATTCTTCTTATTTTCTGGGGCTGTCAGA
TCCAGGGGGGTCGGCGACATTGGCAATGGGTTGACCAGACACCATACAA
TGAAAATGTCACATTCTGGCACTCAGGTGAACCCAATAACCTTGATGA
GCGTTGTGCGATAATAAATTTCCGTTCTTCAGAAGAATGGGGCTGGAAT
GACATTCACCTGTCATGTACCTCAGAAGTCAATTTGCAAGATGAAGAAG
ATCTACATATAAATGAAATATTCTCCCTGGAAATGTGTTTGGGTTGGCA
TCCACCGTTGTAGAAAGCTAAATTGATTTTTTAATTTATGTGTAAGTTTT
GTACAAGGAATGCCCCTAAAATGTTTCAGCAGGCTGTCACCTATTACAC
TTATGATATAATCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
(SEQ ID NO:1)



FIGURE 13

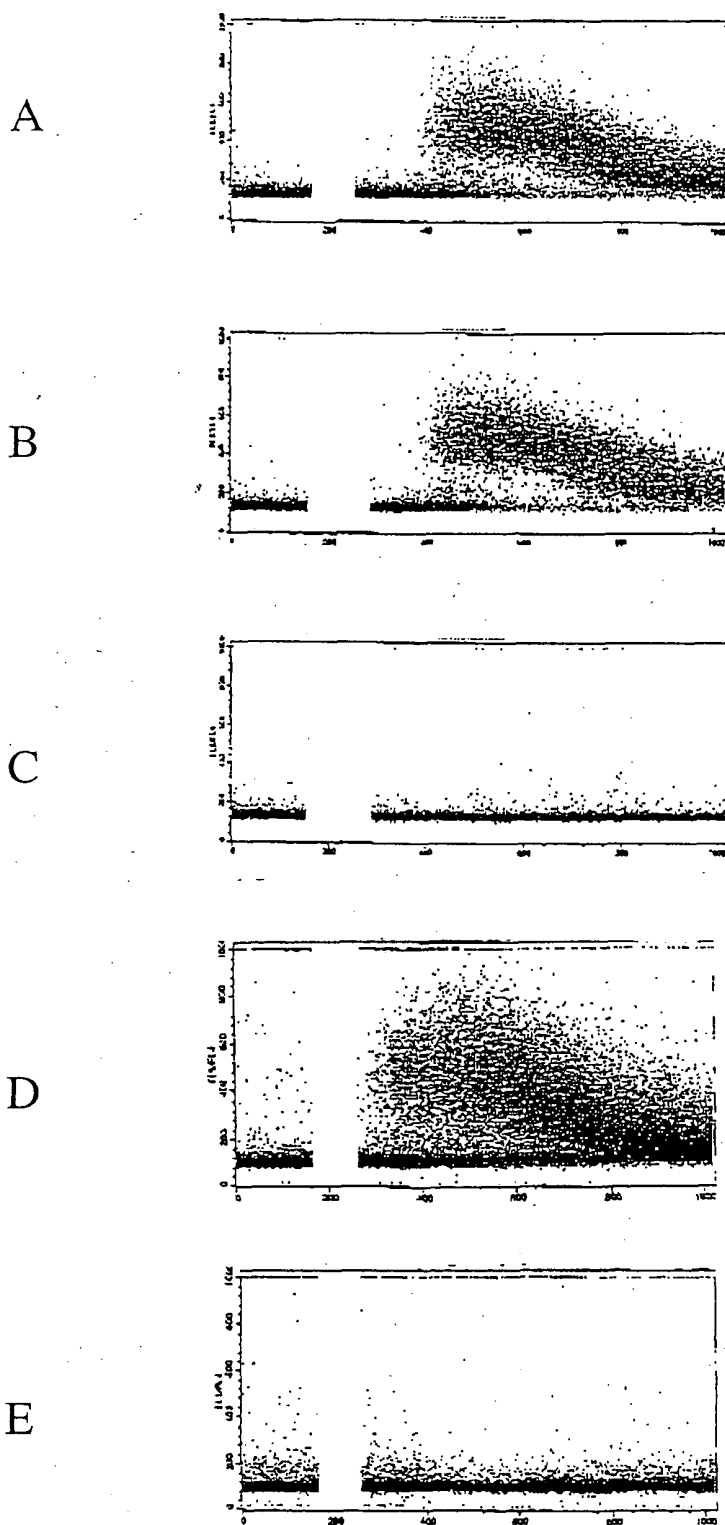
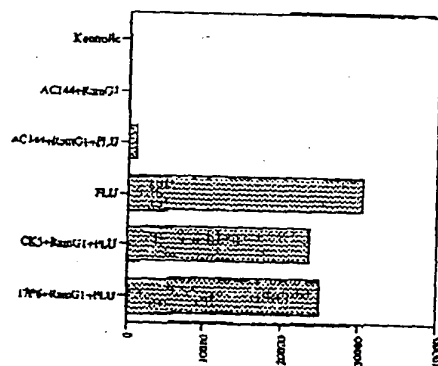


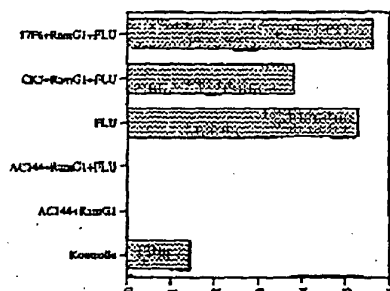
FIGURE 14

A



Type I interferon

B



Type I interferon

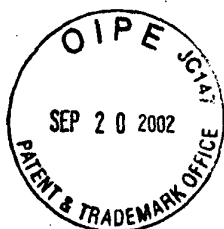


FIGURE 15

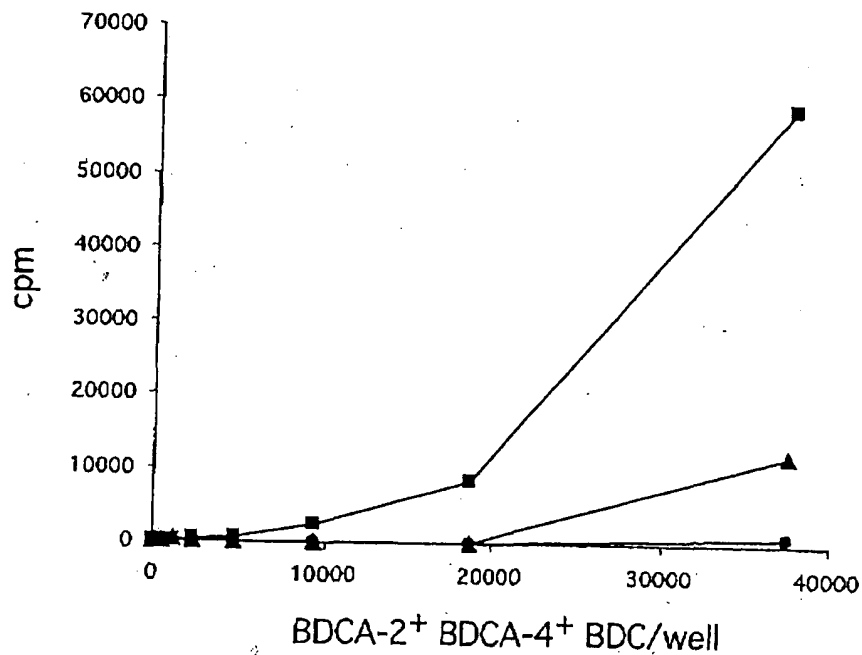


FIGURE 16

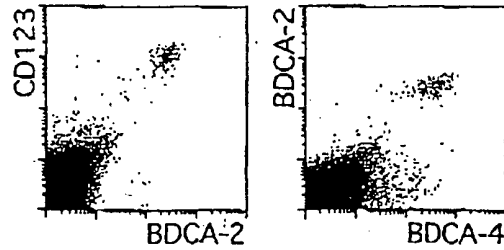


FIGURE 17

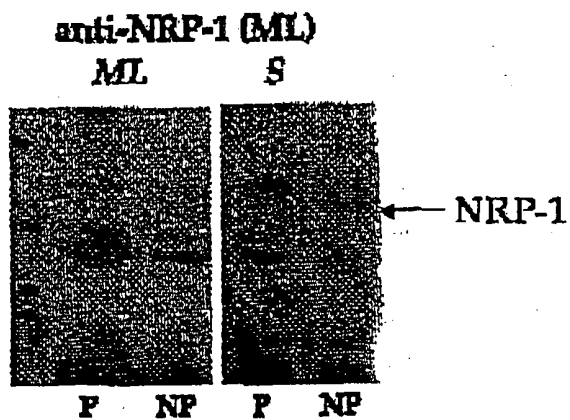


FIGURE 18

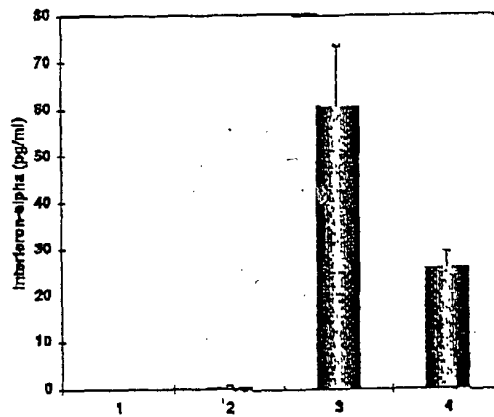


FIGURE 19

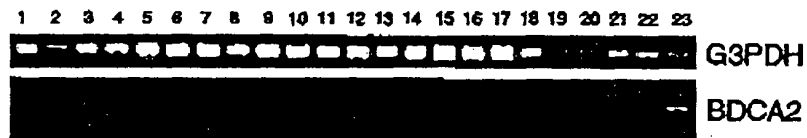


FIGURE 20

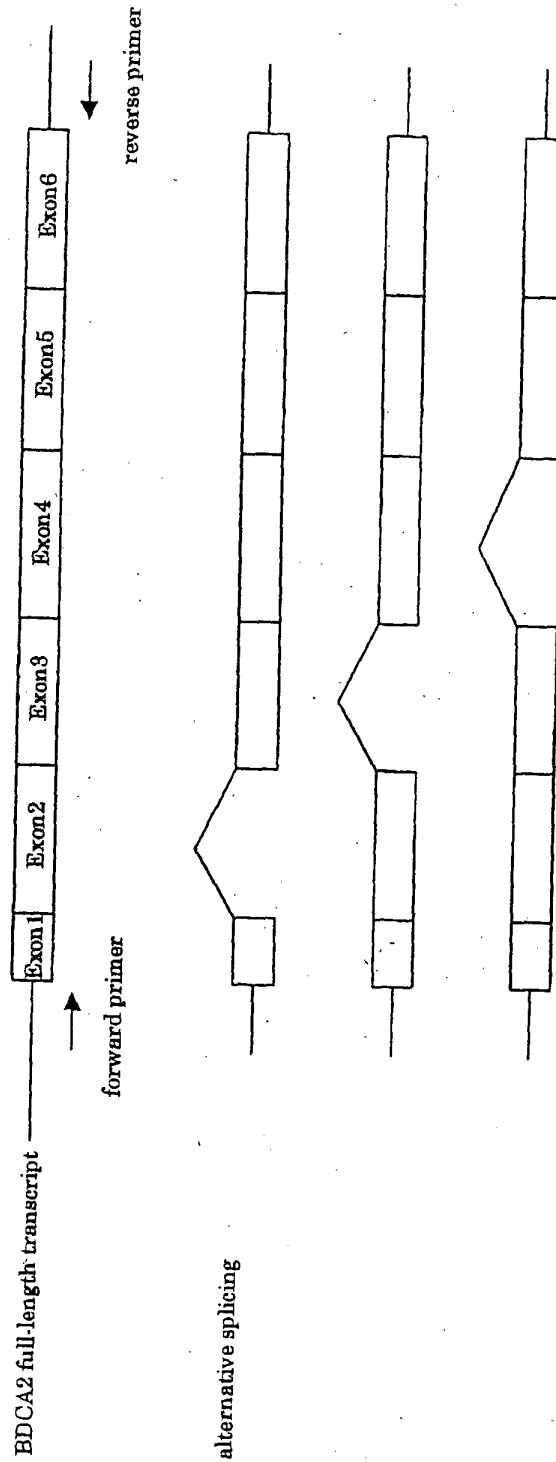
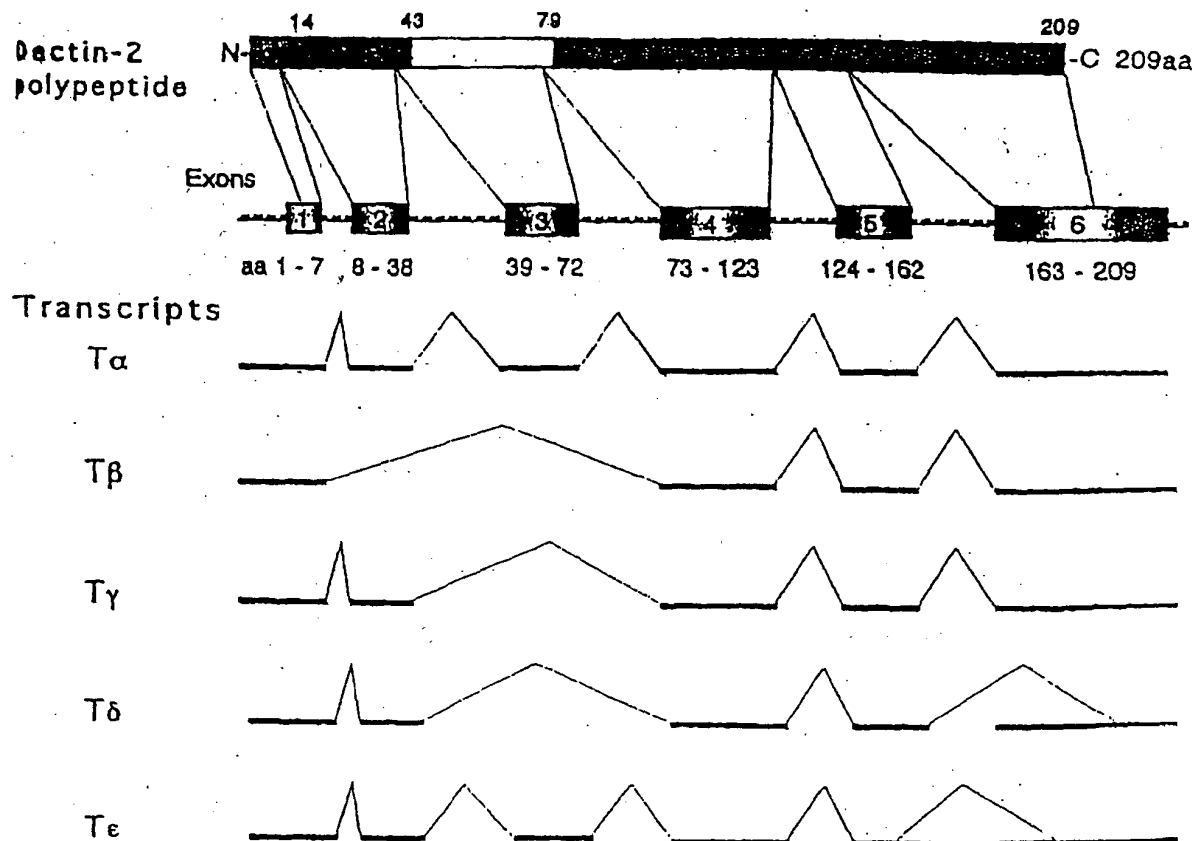


FIGURE 21



1 mDectin2alph

360 370 380 390 400 410
BDCA2cDNA. tx CCTCAGCGCCGGAAGAGGATCTAAGCGCTTGGCTTGTGTGGAAGAACCACACCGCGAA-
mDectin2alph CATTTGGCCCGCTCTGTGGCATTTAA----CTCAAGTGTGTG-TGGAAGTTGATTTCTGAAC
10 20 30 40 50
BDCA2cDNA. tx AGTAACATCTTTG-GAGAA-AGTGATCAAGAG----CTTCTGCACCCACCTGATGAGG
mDectin2alph TCTGGCCCTCTTTGACGAAGCCAGGCTCCCTGAGTGGTATTTTGGAGACAGATGCAAGA--
60 70 80 90 100 110
BDCA2cDNA. tx AAGTCCAAAGGGTGTGGGCACACACATGTGCTGAAGAAGAGCCTCAAGACCCGAGAGA
mDectin2alph AACCCCTGACCTTCTGACATACACCTCAACATGTGTCAGGAAGAACAATCCCAAGCGGA
120 130 140 150 160 170
BDCA2cDNA. tx AAGGACTCTGGTGGTTCCAGTTGAAGGTCTGGTCCATGGCAGTGGTATCCATCTTGTCTCC
mDectin2alph AGGGAGTCTGCTGGACCCCTG---AGACTCTTGGTCACTGCTGTGATTTCCATGTTACTCT
180 190 200 210 220 230
BDCA2cDNA. tx TCAGTGTCTGTTTCACTGTGAGTTCTGTGGTGGCTCACAATTTTATGTATAGCAAAACTG
mDectin2alph TGAATACCTGTTTCAITGCGAGCTGTGTGGTGACTTACCAATTTAT-TAT---GGACCAG
240 250 260 270 280 290
BDCA2cDNA. tx TCAAGAGGCTGTCCAAGTTACGAGAGTATCAACAGTATCATCAAGCCCTGACCTCGGTCA
mDectin2alph CCCAGTAGAAG---ACTATATGA-ACT-TACACATACACTTCCAGTCTCACTGCTTCA
290 300 310 320 330 340
BDCA2cDNA. tx -TGGAAGGA--AAGG--ACATAGAAGT-TGGAGCTGCTGCCAACCCCTTGGACTTTCAT
mDectin2alph GTGAAGGAGTATGGTGTGAGAAATAATGTGGGATGCTGCCAAATCATTGGAAGTCAAT
350 360 370 380 390 400
BDCA2cDNA. tx TTCAGTCTAGTTGCTACTTATTTTCTACTGGGATGCAATCTTGGACTAAGAGTCAAAAGA
mDectin2alph TTGGCTCAGCTGCTACCTCATTTCTACCAAGGAACCTTCTGGAGCACCAGTGAGCAGA
410 420 430 440 450 460
BDCA2cDNA. tx ACTGTTCTGTGATGGGGGCTGATCTGGTGGTGATCAACACAGGGAAGAACAAGATTTC
mDectin2alph ACTGTTCTCAGATGGGGGCTCATCTGGTGGTGATCAATCTGAAGCGAGCAGATTTC
470 480 490 500 510 520
BDCA2cDNA. tx TCATTTCAGAAATCTGAA-AAGAAATCTTCTTATTTTCTGGGGCTGTGAGATCCAGGGGT
mDectin2alph TCACCCAGCAGCTGAATGAGTCACT-TTCTTACTTCTGGGCTTTCGGATCCACAAGGT
530 540 550 560 570 580
BDCA2cDNA. tx CGCGACATTGGCAATGGGTGTGACCAGACACCATAACAATGAAATGTCAATCTGGGCAC
mDectin2alph AATGGCAAAATGGCAATGGATGATGATCTCCCTTTCAGTCAAAATGTCAGTTCTGGAC
590 600 610 620 630 640
BDCA2cDNA. tx TCAGGTGAACCCAATACCTTGATGAGCGTTGTGGGATATAAAATTTCCGTTCTCTAGAA
mDectin2alph CCCCATGAACCCAATCTTCCAGAAGACCGGTGTGTTCAATAGTTTACTGGAAATCCTTCG
650 660 670 680 690 700
BDCA2cDNA. tx GAATGGGGCTGGAATGACATTCACCTGTGATGACCTCAGAGTCAATTTGCAAGATGAAG
mDectin2alph AAATGGGGCTGGAATGATGTTTCTGTGATAGTAAACAAATTCATATGTGAAATGAAG
710 720 730 740 750 760
BDCA2cDNA. tx AAGATTACATATATATGAATATTTCTCCCTGGAAATGTGTTGGGTGGCATCCACCGT
mDectin2alph AAGATTACATATATGATG-CTGTGATTTCAATATCT-TTAAAGTTACAGACTACC--
770 780 790 800 810 820
BDCA2cDNA. tx TGTAGAAAGCTAAATTGATTTTTTAATTTATGTGAAG-TTTTGTACAGGAAT-GCCCC
mDectin2alph --AAGAAGCCATTAATTTCTGGCCCTGTACATCTGACAGAGCCGTTCTTTCTAGCCAC
830 840 850 860 870 880
BDCA2cDNA. tx TAAAATGT--TTACAGAGGCTGTACCTATTACCTTATGATATATCCAAAAA
mDectin2alph TATTTCTTACTCAACAGCAATGAGCCCT-TTCTCTCTGATGGTTAGAGTTTGTCAAC
890 900 910 920 930
BDCA2cDNA. tx AAAAAA (Seq ID No:1)
mDectin2alph TTGACACAACTAGAGTCA (Seq ID No:3)
940 950



FIGURE 23

SEQ ID
NC

BDCA-2	2	MVPEEPQDR--EKGLWNEQLKVWSMAV-----VSILLLSVCFIVS	39
DECTIN-2	4	MVQERQSOG---KGVCTW-LRLWSAAV-----ISMILLSTCFIAS	36
DCIR	5	MTSEITYAEVRFKNEFKSSGINTASSAASKERTAPHSNTGFPKLLCASLIIFFLLLAIS	60
		*. * *	

		C	W	CH	
BDCA-2		SWPHNFMYSKTVKRLSKLREYQQYHPSLTCVMEGKDIED--WSC			97
DECTIN-2		CVVTYQFIMDQPSRRLYEL---HTYRSSLTCFSEGTMVSEKMWGC			93
DCIR		FFIAFVIFPQKYSQLEKKTTELVTHTLECVKKNMPVEETAWSCH			120
	 *			

		A	A	C	A	A	E	HA	ΔAGA +	ΔH	
BDCA-2		[REDACTED]									157
DECTIN-2		[REDACTED]									153
DCIR		[REDACTED]									180
		** * *									

		H	W	+P++	++CA	W++	C	C		
BDCA-2		[REDACTED]							KMKKIYI---	213
DECTIN-2		[REDACTED]							EMKKIYL---	209
DCIR		[REDACTED]							EMMKIHL---	237
		***. . . . *								



FIGURE 24

